



(1) GENERAL INFORMATION

(i) APPLICANTS: Gaugler, B*atrice; Van den Eynde, Benoit; van der Bruggen, Pierre; Boon-Falleur, Thierry

(ii) TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
- (B) STREET: 666 Fifth Avenue
- (C) CITY: New York City
- (D) STATE: New York
- (F) ZIP: 10103

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
- (B) COMPUTER: IBM
- (C) OPERATING SYSTEM: PC-DOS
- (D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/583,848
- (B) FILING DATE: 31-MAY-2000
- (C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US92/04354
- (B) FILING DATE: 22-MAY-1992

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/807,043
- (B) FILING DATE: 12-DECEMBER-1991

(ix) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/764,364
- (B) FILING DATE: 23-SEPTEMBER-1991

(x) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/728,838
- (B) FILING DATE: 9-JULY-1991

(xi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/705,702
- (B) FILING DATE: 23-MAY-1991

(xii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Hanson, Norman D.
- (B) REGISTRATION NUMBER: 30,946
- (C) REFERENCE/DOCKET NUMBER: LUD 5353

(xiii) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 688-9200
- (B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG      60
ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT      120
CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG      180
CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC      240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT      300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGT      360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT      420
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                        462
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(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT      48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
      5              10              15
GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA      96
Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
      20              25              30
GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA      144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
      35              40              45
AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG      192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
      50              55              60
TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC      240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
      65              70              75              80
TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC      288
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
      85              90              95
GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT      336
Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
      100             105             110
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG      384
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
      115             120             125
GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG      432
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
      130             135             140
GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG      480
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Gly	Ala	Gly	Ala	Asn	Cys	Ala	Cys	Val	Pro	Gly	His	His	Leu	Arg	Lys	
145					150					155					160	
AAT	GAA	GTG	AAG	TGT	AGG	ATG	ATT	TAT	TTC	TTC	CAC	GAC	CCT	AAT	TTC	528
Asn	Glu	Val	Lys	Cys	Arg	Met	Ile	Tyr	Phe	Phe	His	Asp	Pro	Asn	Phe	
				165					170					175		
CTG	GTG	TCT	ATA	CCA	GTG	AAC	CCT	AAG	GAA	CAA	ATG	GAG	TGT	AGG	TGT	576
Leu	Val	Ser	Ile	Pro	Val	Asn	Pro	Lys	Glu	Gln	Met	Glu	Cys	Arg	Cys	
			180					185					190			
GAA	AAT	GCT	GAT	GAA	GAG	GTT	GCA	ATG	GAA	GAG	GAA	GAA	GAA	GAA	GAG	624
Glu	Asn	Ala	Asp	Glu	Glu	Val	Ala	Met	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
		195					200				210					
GAG	GAG	GAG	GAG	GAA	GAG	GAA	ATG	GGA	AAC	CCG	GAT	GGC	TTC	TCA	CCT	672
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Met	Gly	Asn	Pro	Asp	Gly	Phe	Ser	Pro	
220					225				230						235	
TAG																675

(2) INFORMATION FOR SEQUENCE ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT	GCAAAGCCCA	GAAGAAAGAA	ATGGACAGCG	GAAGAAGTGG	TTGTTTTTTT	60
TTCCCCTTCA	TTAATTTTCT	AGTTTTTAGT	AATCCAGAAA	ATTTGATTTT	GTTCTAAAGT	120
TCATTATGCA	AAGATGTCAC	CAACAGACTT	CTGACTGCAT	GGTGAACCTT	CATATGATAC	180
ATAGGATTAC	ACTTGACCT	GTAAAAATA	AAAGTTTGAC	TTGCATAC		228

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	50
GAAGATCCTG	ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	100
CAGCCAATGA	GCTTACTGTT	CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	150
AAGTTTTGCA	AGTTCCGCCT	ACAGCTCTAG	CTTGTGAATT	TGTACCCTTT	200
CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	CCCCCTCCCA	250
CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTT	GCTCTCCCAG	350
CATGCATTGT	GTCAACGCCA	TTGCACTGAG	CTGGTCGAAG	AAGTAAGCCG	400
CTAGCTTGCG	ACTCTACTCT	TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	450
ACCCTTTGTG	CC				462

ATG	TCT	GAT	AAC	AAG	AAA	CCA	GAC	AAA	GCC	CAC	AGT	GGC	TCA	504
GGT	GGT	GAC	GGT	GAT	GGG	AAT	AGG	TGC	AAT	TTA	TTG	CAC	CGG	546
TAC	TCC	CTG	GAA	GAA	ATT	CTG	CCT	TAT	CTA	GGG	TGG	CTG	GTC	588
TTC	GCT	GTT	GTC	ACA	ACA	AGT	TTT	CTG	GCG	CTC	CAG	ATG	TTC	630

ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT	924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT	966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG	1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT	1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG	1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	1134
TAG	1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG	1187
TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA	1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
GTTAAAAATA AAAGTTTGAC TTGCATAC	1365

(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4698 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCCTT	200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCCCTCA	250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG	350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
ACCCTTTGTG CC	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T	916
GTGAGTAACC CGTGCTCTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA	966
CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC	1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC	1066
CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC	1116
TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC	1166
TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC	1216
TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCTCCCC TTCTGTTC	1266

CCTTTTCGCG	CCTTTTCTTT	CCTGCTCCCC	TCCCCCTCCC	TATTTACCTT	1316									
TCACCAGCTT	TGCTCTCCCT	GCTCCCCCTCC	CCCTTTTGCA	CCTTTTCTTT	1366									
TCCTGCTCCC	CTCCCCCTCC	CCTCCCTGTT	TACCCTTCAC	CGCTTTTCCT	1416									
CTACCTGCTT	CCCTCCCCCT	TGCTGCTCCC	TCCCTATTTG	CATTTTCGGG	1466									
TGCTCCTCCC	TCCCCCTCCC	CCTCCCTCCC	TATTTGCATT	TTGGGTGCT	1516									
CCTCCCTCCC	CCTCCCCAGG	CCTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	1566									
TTGGTTTTTC	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCCCTGGCAG	1616									
TCACTCTGTA	GACCAGGCTG	GCCTCAAAC	CAGAAATCTG	CCTGCCTCTG	1666									
CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716									
GCCTTTCTTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766									
AACTCCCCTT	TTGGCACCTT	TCCTTTACAG	GACCCCTCC	CCCTCCCTGT	1816									
TTCCCTTCCG	GCACCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866									
CCTCCCCCTC	TTTGCTCGAC	TTTAGCAGC	CTTACCTCTC	CCTGCTTTCT	1916									
GCCCCGTTCC	CCTTTTTTGT	GCCTTTCCTC	CTGGCTCCCC	TCCACCTTCC	1966									
AGCTCACCTT	TTTGTTTGT	TGGTTGTTT	GTTGTTGGT	TTGCTTTTTT	2016									
TTTTTTTTTT	GCACCTGTT	TTCCAAGATC	CCCCTCCCC	TCCGGCTTCC	2066									
CCTCTGTGTG	CCTTTCCTGT	TCCCTCCCC	TCGCTGGCTC	CCCCCTCCCT	2116									
TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166									
CTTTTCTAGA	CTCCCCCTC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216									
CCTGACCCTG	CTCCCCCTCC	CCTCCCAGCT	CCCCCTCTT	TTCCCACCTC	2266									
CCTTTCTCCA	GCCTGTCACC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCACT	2316									
TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366									
GACTTCCTCT	CCAGCCGCC	AGTTCCCTGC	AGTCCTGGAG	TCTTTCCTGC	2416									
CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCCCT	2466									
ATGTGTCTCT	TCTCCTATCT	ATCCCTCCCT	TTCTGTCCCC	TCTCCTCTGT	2516									
CCATCACCTC	TCTCCTCCCT	TCCCTTTCCT	CTCTCTTCCA	TTTTCTTCCA	2566									
CCTGCTTCTT	TACCCTGCCT	CTCCCATTGC	CCTCTTACCT	TTATGCCCAT	2616									
TCCATGTCCC	CTCTCAATTC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666									
ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716									
TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTATG	CCCTCTACTC	2766									
TACTTGATCT	TCTCTCCTCT	CCACATAACC	TTTTTCCTTT	CCACCCTGCC	2816									
CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866									
ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCAA	ATCAGCAGGA	2916									
AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966									
AAGTGGCTCC	TATAACCCCTA	AGTACCAAGG	GAGAAAGTGA	TGGTGAAGTT	3016									
CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066									
CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116									
GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCACG	3166									
TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216									
TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACTATGAA	GTTCTTTTTA	3266									
GGCTAAAGAT	ACTTGGAACC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTCTT	3316									
TTGCTAAAAT	ATTCTTTCTC	ACATATTCAT	ATTCTCCAG		3355									
GT	GTT	CCT	GGC	CAT	CAT	TTA	AGG	AAG	AAT	GAA	GTG	AAG	TGT	3396
AGG	ATG	ATT	TAT	TTC	TTC	CAC	GAC	CCT	AAT	TTC	CTG	GTG	TCT	3438
ATA	CCA	GTG	AAC	CCT	AAG	GAA	CAA	ATG	GAG	TGT	AGG	TGT	GAA	3480
AAT	GCT	GAT	GAA	GAG	GTT	GCA	ATG	GAA	GAG	GAA	GAA	GAA	GAA	3522
GAG	GAG	GAG	GAG	GAG	GAA	GAG	GAA	ATG	GGA	AAC	CCG	GAT	GGC	3564
TTC	TCA	CCT	TAG											3576
GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCCTAACA	TATGCCTGTA										3626
GCTAAGAGCA	TCTTTTTTAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA										3676
TCTTTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTATACA	GTTTTAAGAA										3726
CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT										3776
GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA										3826
GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG										3876
TTCTTATAGT	ACCTTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT										3926
TTCAAGAAAG	ATCACACGCC	ATGGTTCACA	TGCAAAATTAT	TATTTTGTCTG										3976
TTCTGATTTT	TTTCATTCT	AGACCTGTGG	TTTTAAAGAG	ATGAAAATCT										4026

CTTAAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT 4076
TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTAA GATTTCTTAA 4126
AATGTTTTTTT AAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA 4176
GTAAGTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA 4226
GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC 4276
CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC 4326
ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT 4376
ATTTTAGTTT CTCCTTGAGA AACAAATGACA AGACATAAAA TTGGCAAGAA 4426
AGTCAGGAGT GTATTCTAAT AAGTGTGCT TATCTCTTAT TTTCTTCTAC 4476
AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT 4526
TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAAATTTGA 4576
TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT 4626
GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA 4676
AATAAAAGTT TGACTTGCAT AC 4698

(2) INFORMATION FOR SEQUENCE ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe

5

(2) INFORMATION FOR SEQUENCE ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG 50
GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC 100
TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG 150
GGCCCGTGGA TTCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT 200
TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT 250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300
CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT 350
CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCTGAGT ACCCTCTCAC 400
TTCCTCCTTC AGGTTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC 450
CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG 500
TTAGAGTCTC CAAGGTTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT 550
CTCTCCCCAG GCCTGTGGGT CTTTATTGCC CAGCTCCTGC CCACACTCCT 600
GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC 650
ACTGCAAGCC TGAGGAAGCC CTTGAGGCC AACAAGAGGC CCTGGGCCTG 700
GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC 750
CCTGGAGGAG GTGCCCCTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC 800
AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA 850
CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG 900
TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT 950
TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG 1000

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GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA 1050
GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG 1100
TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA 1150
GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC 1200
AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG 1250
CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT 1300
GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA 1350
TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC 1400
CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT 1450
ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT 1500
TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT 1550
CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC 1600
ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG 1650
CCCATTCCTC ACTCTGAAGA GAGCGGTCAG TGTTCTCAGT AGTAGGTTTC 1700
TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT 1750
TCAAATGTTT TTTTAAAGG GATGGTTGAA TGAACCTCAG CATCCAAGTT 1800
TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA 1850
GTCTTGTGTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG 1900
ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA 1950
AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC 2000
CTTATACCTC AGTCTATTCT GTAAATTTT TAAAGATATA TGCATACCTG 2050
GATTTCCCTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG 2100
AATTCCTTCT GTTCACTGGC TCTTTCTTC TCCATGCACT GAGCATCTGC 2150
TTTTTGAAG GCCCTGGGT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT 2200
CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG 2250
AGGTGGCAGC ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA 2300
GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG 2350
GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT 2400
AATGATCTTG GGTGGATCC 2419

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(2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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CCCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT 50
TACGCCACCC ATCCAAACAT CTTACGCTC ACCCCCAGCC CAAGCCAGGC 100
AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG 150
ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT 200
CGGTCTGAGG GGCGGCTTGA GATCGGTGGA GGGGAAGCGG CCCAGCTCTG 250
TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC 300
AGATAGAGGA CCCCAAATAA TCCCTTCATG CCAGTCCTGG ACCATCTGGT 350
GGTGGACTTC TCAGGCTGGG CCACCCCAG CCCCTTGCT GCTTAAACCA 400
CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG 450
AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG 500
AGGGCTGAGG GTCCCTAAGA CCCCCTCCC GTGACCCAAC CCCCCTCCA 550
ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCATT CCAACCCCCA 600
CCCCACATCC CCCACCCCAT CCCTCAACCC TGATGCCCAT CCGCCAGGCC 650
ATTCCACCTT CACCCCCACC CCCACCCCCA CGCCCACTCC CACCCCCACC 700
CAGGCAGGAT CCGGTTCCTG CCAGGAAACA TCCGGGTGCC CGGATGTGAC 750

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GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
AGGGACGGCG	TAGAGTTTCGG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
AGGCAAGGTG	AGAGGCTGAG	GGAGGACTGA	GGACCCCGCC	ACTCCAAATA	900
GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCCACC	950
CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCCC	CCAGACCCCT	GCTCCAAAAG	1000
CCTTGAGAGA	CACCAGGTTT	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
ACTCCAATCC	CCACTCCCAC	CCCA'TTCGCA	TTCCCATTC	CCACCCAACC	1200
CCCATCTCCT	CAGCTACACC	TCCACCCCCA	TCCCTACTCC	TACTCCGTCA	1250
CCTGACCACC	ACCCTCCAGC	CCCAGCACCA	GCCCCAACCC	TTCTGCCACC	1300
TCACCCTCAC	TGCCCCCAAC	CCCACCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
CCCATCGCCT	CCCCCATTC	GGCAGAATCC	GGTTTGCCCC	TGCTCTCAAC	1400
CCAGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCACTGACT	TGAACCTCAC	1450
AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
ATCCACTGAG	GGGAGTGGTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
ATCCAGTACC	ACCCCTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
GTCTCAGCTG	GACCACCCCC	CGTCCCGTCC	CACTGCCACT	TAACCCACAG	1700
GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCGGCAT	TAGGGTCAGG	1800
ACCCTGGGAG	GGAAGTGAAG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
CACCGCCACC	CCACTCACAT	TCCCATACTT	ACCCCTACC	CCCAACCTCA	1900
TCTTGTCAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAGGG	2000
GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050
GGGAGGCCTC	AGAGGACCCA	GCACCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
TTGCATGGGG	GTGGGACCCA	GGCCTGCAAG	GCTTACGCGG	AGGAAGAGGA	2200
GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGGCCCT	2250
GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
CTGTCCCCTT	TTAGTAGCTC	TAGGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
TTCCATTCTC	ACTTGTAACA	CAGGCAGGAA	GTTGGGGGGC	CCTCAGGGAG	2550
ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
GGTTGAGGAA	GCACAGGCGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
AGGCTATTGG	AATCCACACC	CCAGAACCAA	AGGGGTCAGC	CCTGGACACC	2700
TCACCCAGGA	TGTGGCTTCT	TTTTCACTCC	TGTTTCCAGA	TCTGGGGCAG	2750
GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
GAACATGAGG	GAGGACTGAG	GGTACCCAG	GACCAAGAACA	CTGAGGGAGA	2900
CTGCACAGAA	ATCAGCCCTG	CCCCTGCTGT	CACCCCAGAG	AGCATGGGCT	2950
GGGCCGTCTG	CCGAGGTCCT	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
GTCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3100
CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150
AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCTCCT	GTCTTCCAT	3200
TCCTTATCAT	GGATGTGAAC	TCTTGATTTG	GATTTCTCAG	ACCAGCAAAA	3250
GGGCAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3300
CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTCACA	GAGTCCAGCC	3350
CACCTCCTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3400
CTGAGGGCCC	GTGGATTCTT	CTTCTTGAG	CTCCAGGAAC	CAGGCAGTGA	3450
GGCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3500
GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3550
TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3600


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TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC TGAGTACCCT 3650
CTCACTTCTT CCTTCAGGTT TTCAGGGGAC AGGCCAACCC AGAGGACAGG 3700
ATTCCCTGGA GGCCACAGAG GAGCACCAAG GAGAAGATCT GTAAGTAGGC 3750
CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC TCTCACACAC 3800
TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCCAGCT CCTGCCCACA 3850
CTCCTGCCTG CTGCCCTGAC GAGAGTCATC 3880
ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA 3922
GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG 3964
CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC 4006
CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG 4048
AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC 4090
ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA 4132
GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC 4174
CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT 4216
CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA 4258
GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT 4300
CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC 4342
TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC 4384
TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG 4426
CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA 4468
ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT 4510
GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT 4552
GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG 4594
CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC 4636
AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG 4678
GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA 4711
AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC 4750
GCTTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG 4800
GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGACTGGGCC 4850
AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCCTGCC TCGTGTGACA 4900
TGAGGCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTT TCAGTAGTAG 4950
GTTTCTGTTC TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTTGGA 5000
ATTGTTCAAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC 5050
AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG 5100
TAAGAGTCTT GTGTTTTATT CAGATTGGGA AATCCATTCT ATTTTGTGAA 5150
TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT GAAAAATGAG 5200
CAGTAAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCAATT 5250
CTTGCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTAAAG ATATATGCAT 5300
ACCTGGATTT CCTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA 5350
TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT GCACTGAGCA 5400
TCTGCTTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT AAGGTAAGCC 5450
AGACTCATAC CCACCCATAG GGTCGTAGAG TCTAGGAGCT GCAGTCACGT 5500
AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG 5550
GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA 5600
GCTGGGGCAT TTTGGGCTTT GGGAACTGC AGTTCCTTCT GGGGGAGCTG 5650
ATTGTAATGA TCTTGGGTGG ATCC 5674

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(2) INFORMATION FOR SEQUENCE ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCCATCCAGA	TCCCCATCCG	GGCAGAAATCC	GGTTCCACCC	TTGCCGTGAA	50
CCCAGGGAAG	TCACGGGCCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTCGGCG	150
GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCCAA	TTAATCCAGC	250
GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
GCTCAGTCGC	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACCGCAG	350
GGAACTCTGG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTCAGGAC	CCCAAGAGGG	450
GACTGAGGGC	AACCCACCCC	CTACCCTCAC	TACCAATCCC	ATCCCCCAAC	500
ACCAACCCCA	CCCCCATCCC	TCAAACACCA	ACCCACCCC	CAAACCCCAT	550
TCCCATCTCC	TCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCCTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
ACGTTACAT	GTACGGCTAA	GGGAGGGAAG	GGGTTGGGTC	TCGTGAGTAT	700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCCACTG	TACCCCTGTC	800
TCAAACCTGAG	CCACCTTTTC	ATTCAGCCGA	GGGAATCCTA	GGGATGCAGA	850
CCCACTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGAAG	900
AAGAGGGAGG	ACTGAGGGGA	CCTTGAGGTC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTGCAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGGC	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGGACCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCCGGCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTT	TTAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACCACAG	GCAGGAGGTT	GGGGAACCCCT	1250
CAGGGAGATA	AGGTGTTGGT	GTAAAGAGGA	GCTGTCTGCT	CATTTTCAGGG	1300
GGTTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
CCACAGGAGG	CCATCATAAC	GTTCAACCCTA	GAACCAAAGG	GGTCAGCCCT	1400
GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTTGTCTTTC	1450
CAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
ACAGGGGCCC	CTCTGGTCGA	CAGATGCAGT	GGTTCTAGGA	TCTGCCAAGC	1550
ATCCAGGTGG	AGAGCCTGAG	GTAGGATTGA	GGGTACCCCT	GGGCCAGAAT	1600
GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCCTGCG	GTTACTTCAG	1650
AGACCCTGGG	CAGGGCTGTC	AGCTGAAGTC	CCTCCATTAT	CTGGGATCTT	1700
TGATGTCAGG	GAAGGGGAGG	CCTTGGTCTG	AAGGGGCTGG	AGTCAGGTCA	1750
GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTTGAC	ATCTCTCGTT	1850
GTCTTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCCTCA	1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
CCTGAGTGAG	CACAGAGGGG	ACCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
GCAGTCTGCA	CACTGAAGGC	CCGTGCATTC	CTCTCCCAGG	AATCAGGAGC	2150
TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCAC	2200
AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
GCCTCACCCCT	CCCTATTCTC	AGTCCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
CTGTACCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTT	TGAGGGGGAC	2400
AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTGA	AGGAGAAGAT	2450
CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
CCCAGCTCCT	GCCCCGACTC	CTGCCTGCTG	CCCTGACCAG	AGTCATC	2597
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723

TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC	2765
GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC	2807
TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT	2849
GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT	2891
CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG	2933
ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	2975
AGG GAG CCG GTC ACA AAG GCA ATG CTG GAG AGT GTC CTC	3017
AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC	3059
TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA	3101
GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG	3143
GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG	3185
CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	3227
ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	3269
CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GAC AGT GTC	3311
TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG	3353
GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT	3395
GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA	3437
ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT	3479
GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT	3521
TTG AGA GAG GGA GAA GAG TGA	3542
GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	3592
GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA	3642
GGCCCATTC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG	3692
TTTCTGTTCT GTTGGATGAC TTTGAGATT ATCTTTCTTT CCTGTTGGAA	3742
TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACCT CAGCATCCAA	3792
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG	3842
TAAGAGTCCT GTTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG	3892
TTGTCACATA ATAACAGCAG TGAATATGT ATTTGCCTAT ATTGTGAACG	3942
AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT	3992
TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT	4042
TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT	4092
TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC	4142
CCTGGTAGTA GTGGG	4157

(2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 662 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-21 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT GGATCCAGGA AGAATCCAGT TCCACCCCTG CTGTGAACCC	50
AGGGAAGTCA CGGGGCCGGA TGTGACGCCA CTGACTTGCG CGTTGGAGGT	100
CAGAGAACAG CGAGATTCTC GCCCTGAGCA ACGGCCTGAC GTCGGCGGAG	150
GGAAGCAGGC GCAGGCTCCG TGAGGAGGCA AGGTAAGATG CCGAGGGAGG	200
ACTGAGGCGG GCCTCACCCC AGACAGAGGG CCCCCAATAA TCCAGCGCTG	250
CCTCTGCTGC CAGGCCTGGA CCACCCTGCA GGGGAAGACT TCTCAGGCTC	300
AGTCGCCACC ACCTCACCCC GCCACCCCCC GCCGCTTTAA CCGCAGGGAA	350
CTCTGGTGTA AGAGCTTTGT GTGACCAGGG CAGGGCTGGT TAGAAGTGCT	400
CAGGGCCCAG ACTCAGCCAG GAATCAAGGT CAGGACCCCA AGAGGGGACT	450
GAGGGTAACC CCCCCGACC CCCACCACCA TTCCCATCCC CCAACACCAA	500
CCCCACCCCC ATCCCCCAAC ACCAAACCCA CCACCATCGC TCAAACATCA	550

ACGGCACCCC CAAACCCCGA TTCCCATCCC CACCCATCCT GGCAGAATCG	600
GAGCTTTGCC CCTGCAATCA ACCCACGGAA GCTCCGGGAA TGGCGGCCAA	650
GCACGCGGAT CC	662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: cDNA MAGE-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG	50
GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA	100
AGATCTGCCA GTGGGTCTCC ATTGCCCAGC TCCTGCCCAC ACTCCCGCCT	150
GTTGCCCTGA CCAGAGTCAT C	171
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	213
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	255
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT	297
TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC	339
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	381
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	423
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	465
CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG	507
GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	549
AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC	591
GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT	633
TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA	675
GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG	717
GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG	759
CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	801
AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	843
CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG	885
TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG	927
GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT	969
GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA	1011
ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT	1053
GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT	1095
TTG AGA GAG GGG GAA GAG TGA	1116
GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	1166
GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA	1216
GGCCCATTTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG	1266
TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG	1316
TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG	1366
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG	1416
TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA	1466
TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC	1516
GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG	1566
ATTCTTGCC TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA	1616
ACCAGGATTT CCTTGACTTC TTTG	1640

(2) INFORMATION FOR SEQUENCE ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 943 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: MAGE-31 gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

GGATCCTCCA CCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT      50
CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG      100
GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG      150
AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA      200
GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC      250
CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT      300
TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC      350
CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC      400
AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG      450
TTAGAGCCTC CAAGGTTCCT TTCAGTACTC AGCTGAGGTC TCTCACATGC      500
TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCTGCCCCACA      550
CTCCCGCCTG TTGCCCTGAC CAGAGTCATC                               580
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA      622
GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG      664
CAG GCT CTT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT      706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC      748
GAG TCA CCA GAT CCT CCC CAg AGT CCT CAG GGA GCC TCC AGC      790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT      832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC      874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG      916
GTG GcC AAG TTG GTT CAT TTT CTG CTC                               943

```

- (2) INFORMATION FOR SEQUENCE ID NO: 13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-4 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG      50
GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC      100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG      150
GGCCCATGGA TTCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT      200
TGGTCTGAGA CAGTGTCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT      250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA      300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT      350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA      400
CTTCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC      450
TGGAGGCCAC AGAGGAGCAC CAAGGAGAAAG ATCTGTAAGT AAGCCTTTGT      500
TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC      550
TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG      600
CCTGCTGCCC TGACCAGAGT CATC                               624

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ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	666
GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA	708
CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC	750
TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT	792
GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT	834
GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC	876
AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC	918
TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC	960
AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA	1002
GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC	1044
ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA	1086
GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG	1128
GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC	1170
CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC	1212
TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT	1254
GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG	1296
GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT	1338
GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG	1380
CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT	1422
CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT	1464
GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC	1506
AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA	1548
GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA	1578
GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC	1628
ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC	1678
CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTCTTA GTAGTGGGTT	1728
TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT	1778
GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT	1828
TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG	1878
AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG	1928
GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT	1978
GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA	2028
GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCCTTG	2078
CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA	2128
ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC	2178
AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA	2228
GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT	2278
CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT	2328
GAGAGTGGTC GGGTGTAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA	2378
AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC	2428
AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC	2478
TCTGAGCAGT TCCTTTTGTA CAATGGATGA ACAGAGAGGA GCCTCTACCT	2528
GGG	2531

(2) INFORMATION FOR SEQUENCE ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-41 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG

50

GGGATCATCC	ACTCCATGAG	AGTGGGGACC	TCACAGAGTC	CAGCCTACCC	100
TCTTGATGGC	ACTGAGGGAC	CGGGGCTGTG	CTTACAGTCT	GCACCCTAAG	150
GGCCCATGGA	TTCCTCTCCT	AGGAGCTCCA	GGAACAAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTGTCTCT	AGGTTACAGA	GCAGAGGATG	CACAGGCTGT	250
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAAGACACAT	AGGACTCCAA	AGAGTCTGGC	CTCACCTCCC	TACCATCAAT	350
CCTGCAGAAT	CGACCTCTGC	TGGCCGGCTA	TACCCTGAGG	TGCTCTCTCA	400
CTTCCTCCTT	CAGGTTCTGA	GCAGACAGGC	CAACCGGAGA	CAGGATTCCC	450
TGGAGGCCAC	AGAGGAGCAC	CAAGGAGAAG	ATCTGTAAGT	AAGCCTTTGT	500
TAGAGCCTCT	AAGATTTGGT	TCTCAGCTGA	GGTCTCTCAC	ATGCTCCCTC	550
TCTCCGTAGG	CCTGTGGGTC	CCCATTGCC	AGCTTTTGCC	TGCACTCTTG	600
CCTGCTGCCC	TGAGCAGAGT	CATC			624
ATG TCT TCT	GAG CAG AAG	AGT CAG CAC	TGC AAG CCT	GAG GAA	666
GGC GTT GAG	GCC CAA GAA	GAG GCC CTG	GGC CTG GTG	GGT GCG	708
CAG GCT CCT	ACT ACT GAG	GAG CAG GAG	GCT GCT GTC	TCC TCC	750
TCC TCT CCT	CTG GTC CCT	GGC ACC CTG	GAG GAA GTG	CCT GCT	792
GCT GAG TCA	GCA GGT CCT	CCC CAG AGT	CCT CAG GGA	GCC TCT	834
GCC TTA CCC	ACT ACC ATC	AGC TTC ACT	TGC TGG AGG	CAA CCC	876
AAT GAG GGT	TCC AGC AGC	CAA GAA GAG	GAG GGG CCA	AGC ACC	918
TCG CCT GAC	GCA GAG TCC	TTG TTC CGA	GAA GCA CTC	AGT AAC	960
AAG GTG GAT	GAG TTG GCT	CAT TTT CTG	CTC CGC AAG	TAT CGA	1002
GCC AAG GAG	CTG GTC ACA	AAG GCA GAA	ATG CTG GAG	AGA GTC	1044
ATC AAA AAT	TAC AAG CGC	TGC TTT CCT	GTG ATC TTC	GGC AAA	1086
GCC TCC GAG	TCC CTG AAG	ATG ATC TTT	GGC ATT GAC	GTG AAG	1128
GAA GTG GAC	CCC ACC AGC	AAC ACC TAC	ACC CTT GTC	ACC TGC	1170
CTG GGC CTT	TCC TAT GAT	GGC CTG CTG	GGT AAT AAT	CAG ATC	1212
TTT CCC AAG	ACA GGC CTT	CTG ATA ATC	GTC CTG GGC	ACA ATT	1254
GCA ATG GAG	GGC GAC AGC	GCC TCT GAG	GAG GAA ATC	TGG GAG	1296
GAG CTG GGT	GTG ATG GGG	GTG TAT GAT	GGG AGG GAG	CAC ACT	1338
GTC TAT GGG	GAG CCC AGG	AAA CTG CTC	ACC CAA GAT	TGG GTG	1380
CAG GAA AAC	TAC CTG GAG	TAC CGG CAG	GTA CCC GGC	AGT AAT	1422
CCT GCG CGC	TAT GAG TTC	CTG TGG GGT	CCA AGG GCT	CTG GCT	1464
GAA ACC AGC	TAT GTG AAA	GTC CTG GAG	CAT GTG GTC	AGG GTC	1506
AAT GCA AGA	GTT CGC ATT	GCC TAC CCA	TCC CTG CGT	GAA GCA	1548
GCT TTG TTA	GAG GAG GAA	GAG GGA GTC	TGA		1578
GCATGAGTTG	CAGCCAGGGC	TGTGGGGAAG	GGGCAGGGCT	GGGCCAGTGC	1628
ATCTAACAGC	CCTGTGCAGC	AGCTTCCCTT	GCCTCGTGTA	ACATGAGGCC	1678
CATTCTTCAC	TCTGTTTGAA	GAAAAAGTGC	AGTGTTCTTA	GTAGTGGGTT	1728
TCTATTTTGT	TGGATGACTT	GGAGATTTAT	CTCTGTTTCC	TTTTACAATT	1778
GTTGAAATGT	TCCTTTTAAT	GGATGGTTGA	ATTAACCTCA	GCATCCAAGT	1828
TTATGAATCG	TAGTTAACGT	ATATTGCTGT	TAATATAGTT	TAGGAGTAAG	1878
AGTCTTGTTT	TTTATTGAGA	TTGGGAAATC	CGTTCTATTT	TGTGAATTTG	1928
GGACATAATA	ACAGCAGTGG	AGTAAGTATT	TAGAAGTGTG	AATTACCCGT	1978
GAAATAGGTG	AGATAAAATTA	AAAGATACTT	AATTCCCGCC	TTATGCCTCA	2028
GTCTATTCTG	TAAAATTTAA	AAATATATAT	GCATACCTGG	ATTTCCCTTG	2078
CTTCGTGAAT	GTAAGAGAAA	TTAAATCTGA	ATAAATAATT	CTTTCTGTTA	2128
ACTGGCTCAT	TTCTTCTCTA	TGCACTGAGC	ATCTGCTCTG	TGGAAGGCCC	2178
AGGATTAGTA	GTGGAGATAC	TAGGGTAAGC	CAGACACACA	CCTACCGATA	2228
GGGTATTAAG	AGTCTAGGAG	CGCGGTCATA	TAATTAAGGT	GACAAGATGT	2278
CCTCTAAGAT	GTAGGGGAAA	AGTAACGAGT	GTGGGTATGG	GGCTCCAGGT	2328
GAGAGTGGTC	GGGTGTAAAT	TCCCTGTGTG	GGGCCTTTTG	GGCTTTGGGA	2378
AACTCCATTT	TCTTCTGAGG	GATCTGATTC	TAATGAAGCT	TGGTGGGTCC	2428
AGGGCCAGAT	TCTCAGAGGG	AGAGGGGAAA	GCCCAGATTG	GAAAAGTTGC	2478
TCTGAGCGGT	TCCTTTGTGA	CAATGGATGA	ACAGAGAGGA	GCCTCTACCT	2528
GGG					2531

(2) INFORMATION FOR SEQUENCE ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1068 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: cDNA MAGE-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```
G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA      40
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG      82
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA     124
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT     166
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT     208
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC     250
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG     292
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC     334
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG     376
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT     418
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC     460
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG     502
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT     544
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG     586
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA     628
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC     670
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG     720
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG     770
GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG     820
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA     870
ATTGTTGAAA TGTTCTTTT AATGGATGGT TGAATTAAT TCAGCATCCA     920
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT     970
AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT    1020
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC      1068
```

(2) INFORMATION FOR SEQUENCE ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2226 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-5 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```
GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG      50
GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC     100
TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG     150
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT     200
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC     250
TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC     300
GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG     350
TCAGTCTTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT     400
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG     450
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GAAGCTCCAG	AGGATCCCCA	GGAGGCCCTA	GAGGAGCACC	AAAGGAGAAG	500
ATCTGTAAGT	AAGCCTTTGT	TAGAGCCTCC	AAGGTTCACT	TTTCTAGCTGA	550
GGCTTCTCAC	ATGCTCCCTC	TCTCTCCAGG	CCAGTGGGTC	TCCATTGCCC	600
AGCTCCTGCC	CACACTCCTG	CCTGTTGCGG	TGACCAGAGT	CGTC	644
ATG TCT CTT	GAG CAG AAG	AGT CAG CAC	TGC AAG CCT	GAG GAA	686
CTC CTC TGG	TCC CAG GCA	CCC TGG GGG	AGG TGC CTG	CTG CTG CTG	728
GGT CAC CAG	GTC CTC TCA	AGA GTC CTC	AGG GAG CCT	CCG CCA	770
TCC CCA CTG	CCA TCG ATT	TCA CTC TAT	GGA GGC AAT	CCA TTA	812
AGG GCT CCA	GCA ACC AAG	AAG AGG AGG	GGC CAA GCA	CCT CCC	854
CTG ACC CAG	AGT CTG TGT	TCC GAG CAG	CAC TCA GTA	AGA AGG	896
TGG CTG ACT	TGA				908
TTCATTTTCT	GCTCCTCAAG	TATTAAGTCA	AGGAGCTGGT	CACAAAGGCA	958
GAAATGCTGG	AGAGCGTCAT	CAAAAATTAC	AAGCGCTGCT	TTCTGAGAT	1008
CTTCGGCAAA	GCCTCCGAGT	CCTTGCAGCT	GGTCTTTGGC	ATTGACGTGA	1058
AGGAAGCGGA	CCCCACCAGC	AACACCTACA	CCCTTGTCAC	CTGCCTGGGA	1108
CTCCTATGAT	GGCCTGCTGG	TTGATAATAA	TCAGATCATG	CCCAAGACGG	1158
GCCTCCTGAT	AATCGTCTTG	GGCATGATTG	CAATGGAGGG	CAAATGCGTC	1208
CCTGAGGAGA	AAATCTGGGA	GGAGCTGAGT	GTGATGAAGG	TGTATGTTGG	1258
GAGGGAGCAC	AGTGTCTGTG	GGGAGCCCAG	GAAGCTGCTC	ACCCAAGATT	1308
TGGTGACAGGA	AAACTACCTG	GAGTACCGGC	AGGTGCCCAG	CAGTGATCCC	1358
ATATGCTATG	AGTTACTGTG	GGGTCCAAGG	GCACTCGCTG	CTTGAAAGTA	1408
CTGGAGCACG	TGGTCAGGGT	CAATGCAAGA	GTTCTCATTT	CCTACCCATC	1458
CCTGCGTGAA	GCAGCTTTGA	GAGAGGAGGA	AGAGGGAGTC	TGAGCATGAG	1508
CTGCAGCCAG	GGCCACTGCG	AGGGGGGCTG	GGCCAGTGCA	CCTTCCAGGG	1558
CTCCGTCCAG	TAGTTTCCCC	TGCCCTTAATG	TGACATGAGG	CCCATTCTTC	1608
TCTCTTTGAA	GAGAGCAGTC	AACATTCTTA	GTAGTGGGTT	TCTGTTCTAT	1658
TGGATGACTT	TGAGATTTGT	CTTTGTTTCC	TTTTGGAATT	GTTCAAATGT	1708
TTCTTTTAAT	GGGTGGTTGA	ATGAACTTCA	GCATTCAAAT	TTATGAATGA	1758
CAGTAGTCAC	ACATAGTGCT	GTTTATATAG	TTTAGGAGTA	AGAGTCTTGT	1808
TTTTTATTCA	GATTGGGAAA	TCCATTCCAT	TTTGTGAATT	GGGACATAGT	1858
TACAGCAGTG	GAATAAGTAT	TCATTTAGAA	ATGTGAATGA	GCAGTAAAC	1908
TGATGACATA	AAGAAATTAA	AAGATATTTA	ATTCTTGCTT	ATACTCAGTC	1958
TATTCGTAA	AATTTTTTTT	AAAAAATGTG	CATACCTGGA	TTCTCTTGGC	2008
TTCTTTGAGA	ATGTAAGACA	AATTAAATCT	GAATAAATCA	TTCTCCCTGT	2058
TCACTGGCTC	ATTTATTCTC	TATGCACTGA	GCATTTGCTC	TGTGGAAGGC	2108
CCTGGGTTAA	TAGTGGAGAT	GCTAAGGTAA	GCCAGACTCA	CCCCTACCCA	2158
CAGGGTAGTA	AAGTCTAGGA	GCAGCAGTCA	TATAATTAAG	GTGGAGAGAT	2208
GCCCTCTAAG	ATGTAGAG				2226

(2) INFORMATION FOR SEQUENCE ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-51 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGATCCAGGC	CTTGCCAGGA	GAAAGGTGAG	GGCCCTGTGT	GAGCACAGAG	50
GGGACCATTC	ACCCAAGAG	GGTGGAGACC	TCACAGATTC	CAGCCTACCC	100
TCCTGTTAGC	ACTGGGGGCC	TGAGGCTGTG	CTTGCACTCT	GCACCTTGAG	150
GGCCCATGCA	TTCTCTTCC	AGGAGCTCCA	GGAAACAGAC	ACTGAGGCCT	200
TGGTCTGAGG	CCGTGCCCTC	AGGTCACAGA	GCAGAGGAGA	TGCAGACGTC	250
TAGTGCCAGC	AGTGAACGTT	TGCCTTGAAT	GCACACTAAT	GGCCCCCATC	300

GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG	350
TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT	400
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG	450
GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG	500
ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA	550
GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC	600
AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC	644
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	686
GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC	728
AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT	770
CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG	812
GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA	854
TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA	896
AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC	938
CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG	980
TGG CTG ACT TGA	992
TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA	1042
GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT	1092
CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA	1142
AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA	1192
CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCTC	1242
CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA	1292
GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG	1342
AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTGTTG	1392
CAGGAAAAC ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC	1442
TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG	1492
CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCTTACC CATCCCTGCA	1542
TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG	1592
CCAGGGCCAC TGCAGGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT	1642
CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCAT CTTCTCTCTT	1692
TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTCTCTGTT CTATTGGATG	1742
ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCTTTT	1792
TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA ATGACAGTAG	1842
TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA	1892
TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC	1942
AGTGAATAAA GTATTTCATTT AGAAATGTGA ATGAGCAGTA AAACCTGATGA	1992
GATAAAGAAA TTAAGAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC	2042
GGTAAATTT TTTTTTAAAA ATGTGCATAC CTGGATTTC TTTGGCTTCTT	2092
TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT	2142
GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG	2192
GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCACAGGG	2242
TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT	2292
CTAAGATGTA GAG	2305

(2) INFORMATION FOR SEQUENCE ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-6 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG

42

GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA 1914
AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG 1947

(2) INFORMATION FOR SEQUENCE ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-8 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GAGCTCCAGG AACCAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA 50
TCACAGAGCA TAAGAGGCCC AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT 100
GTTTCCCCTG TATGTATACC AGAGGCCCTT CTGGCATCAG AACAGCAGGA 150
ACCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCAGTCC TGGAGCCTTG 200
GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA 250
GGTTCGAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGAGAAGCA 300
CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA 350
CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT 400
CAATTGCCCC GCTCCGGCCC AACTCTCTCT GCTGCCCTGA CCTGAGTCAT 450
C 451
ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA 493
GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG 535
CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC 577
TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT 619
GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT 661
TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT 703
GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC 745
CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT 787
GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA 829
TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG 871
AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC 913
AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT 955
GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC 997
ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT 1039
CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC 1081
ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC 1123
TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA 1156
TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG 1206
AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT 1256
CCTGTGCGCT ACGAGTTTCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG 1306
CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA 1356
TTTCCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT 1406
TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTGTG GGAGGGCCTG 1456
GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTCCCT GCTCTGTTAC 1506
ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA 1556
GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC 1606
AGTTCTGTG CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG 1656
AATTGTTCCA ATGTTCTTTC TAATGGATGG TGTAATGAAC TTCAACATTC 1706
ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTATA TAGTTTAGGA 1756
GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA 1806
ATTC 1810

(2) INFORMATION FOR SEQUENCE ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-9 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```
TCTGAGACAG TGTCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC 50
AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT 100
GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG 150
TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC 200
TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA 250
GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT 300
TGTTAGAACC TCCAAGGTTC GGTTCTCAGC TGAAGTCTCT CACACACTCC 350
CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCCAGGCTC 400
CTGACTGCTG CCCTGACCAG AGTCATC 427
ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA 469
GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA 511
CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT 553
GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT 595
CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC 637
GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC 679
AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT 721
CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG 763
GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG 805
GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA 847
AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC 889
GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG 931
GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC 973
CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC 1015
AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC 1057
AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG 1099
AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC 1141
GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA 1183
AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG 1225
CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC 1267
AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA 1309
AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG 1351
GGA GAG GAG CAA GAG GGA GTC TGA 1375
GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA 1412
```

(2) INFORMATION FOR SEQUENCE ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-10 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ACCTGCTCCA	GGACAAAGTG	GACCCCACTG	CATCAGCTCC	ACCTACCCTA	50
CTGTCACTCC	TGGAGCCTTG	GCCTCTGCCG	GCTGCATCCT	GAGGAGCCAT	100
CTCTCACTTC	CTTCTTCAGG	TTCTCAGGGG	ACAGGGAGAG	CAAGAGGTCA	150
AGAGCTGTGG	GACACCACAG	AGCAGCACTG	AAGGAGAAGA	CCTGTAAGTT	200
GGCCTTTGTT	AGAACCTCCA	GGGTGTGGTT	CTCAGCTGTG	GCCACTTACA	250
CCCTCCCTCT	CTCCCCAGGC	CTGTGGGTCC	CCATCGCCCA	AGTCCTGCCC	300
ACACTCCCAC	CTGCTACCCT	GATCAGAGTC	ATC		333
ATG CCT CGA	GCT CCA AAG	CGT CAG CGC	TGC ATG CCT	GAA GAA	375
GAT CTT CAA	TCC CAA AGT	GAG ACA CAG	GGC CTC GAG	GGT GCA	417
CAG GCT CCC	CTG GCT GTG	GAG GAG GAT	GCT TCA TCA	TCC ACT	459
TCC ACC AGC	TCC TCT TTT	CCA TCC TCT	TTT CCC TCC	TCC TCC	501
TCT TCC TCC	TCC TCC TGC	TAT CCT CTA	ATA CCA AGC	ACC	543
CCA GAG GAG	GTT TCT GCT	GAT GAT GAG	ACA CCA AAT	CCT CCC	585
CAG AGT GCT	CAG ATA GCC	TGC TCC TCC	CCC TCG GTC	GTT GCT	627
TCC CTT CCA	TTA GAT CAA	TCT GAT GAG	GGC TCC AGC	AGC CAA	669
AAG GAG GAG	AGT CCA AGC	ACC CTA CAG	GTC CTG CCA	GAC AGT	711
GAG TCT TTA	CCC AGA AGT	GAG ATA GAT	GAA AAG GTG	ACT GAT	753
TTG GTG CAG	TTT CTG CTC	TTC AAG TAT	CAA ATG AAG	GAG CCG	795
ATC ACA AAG	GCA GAA ATA	CTG GAG AGT	GTC ATA AAA	AAT TAT	837
GAA GAC CAC	TTC CCT TTG	TTG TTT AGT	GAA GCC TCC	GAG TGC	879
ATG CTG CTG	GTC TTT GGC	ATT GAT GTA	AAG GAA GTG	GAT CC	920

(2) INFORMATION FOR SEQUENCE ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-11 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AGAGAACAGG	CCAACCTGGA	GGACAGGAGT	CCCAGGAGAA	CCCAGAGGAT	50
CACTGGAGGA	GAACAAGTGT	AAGTAGGCCCT	TTGTTAGATT	CTCCATGGTT	100
CATATCTCAT	CTGAGTCTGT	TCTCACGCTC	CCTCTCTCCC	CAGGCTGTGG	150
GGCCCCATCA	CCCAGATATT	TCCCACAGTT	CGGCCTGCTG	ACCTAACCAG	200
AGTCATCATG	CCTCTTGAGC	AAAGAAGTCA	GCACTGCAAG	CCTGAGGAAG	250
CCTTCAGGCC	CAAGAAGAAG	ACCTGGGCCCT	GCTGGGTGCA	CAGGCTCTCC	300
AAGCTGAGGA	GCAGGAGGCT	GCCTTCTTCT	CCTCTACTCT	GAATGTGGGC	350
ACTCTAGAGG	AGTTGCCTGC	TGCTGAGTCA	CCAAGTCCTC	CCCAGAGTCC	400
TCAGGAAGAG	TCCTTCTCTC	CCACTGCCAT	GGATGCCATC	TTTGGGAGCC	450
TATCTGATGA	GGGCTCTGGC	AGCCAAGAAA	AGGAGGGGCC	AAGTACCTCG	500
CCTGACCTGA	TAGACCCTGA	GTCTTTTCC	CAAGATATAC	TACATGACAA	550
GATAATTGAT	TTGGTTCATT	TATTCTCCGC	AAGTATCGAG	TCAAGGGGCT	600
GATCACAAAG	GCAGAA				616
ATG CTG GGG	AGT GTC ATC	AAA AAT TAT	GAG GAC TAC	TTT CCT	658
GAG ATA TTT	AGG GAA GCC	TCT GTA TGC	ATG CAA CTG	CTC TTT	700
GGC ATT GAT	GTG AAG GAA	GTG GAC CCC	ACT AGC CAC	TCC TAT	742
GTC CTT GTC	ACC TCC CTC	AAC CTC TCT	TAT GAT GGC	ATA CAG	784
TGT AAT GAG	CAG AGC ATG	CCC AAG TCT	GGC CTC CTG	ATA ATA	826
GTC CTG GGT	GTA ATC TTC	ATG GAG GGG	AAC TGC ATC	CCT GAA	868
GAG GTT ATG	TGG GAA GTC	CTG AGC ATT	ATG GGG GTG	TAT GCT	910
GGA AGG GAG	CAC TTC CTC	TTT GGG GAG	CCC AAG AGG	CTC CTT	952
ACC CAA AAT	TGG GTG CAG	GAA AAG TAC	CTG GTG TAC	CGG CAG	994

GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT	1036
CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG	1078
TAC ATA GCC AAT GCC AAT GGG AGG GAT CC	1107

(2) INFORMATION FOR SEQUENCE ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: smage-I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TCTGTCTGCA TATGCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT	50
CTCTACAGAC CTCTGTCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC	100
ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC	150
TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT	200
GCCCTTGAT GCAGGCCTAA GTTTTCTGT CTGCTTAACC CCTCCAAGTG	250
AAGCTAGTGA AAGATCTAAC CCACTTTTGG AAGTCTGAAA CTAGACTTTT	300
ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG	350
AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTTCCTAG AAAG	394
ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT	436
CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT	478
TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT	520
ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG	562
AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG	604
GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT	646
TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT	688
TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA	730
GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT	772
GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA	814
GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG	856
AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG	898
ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT	940
AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA	982
ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG	1024
GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA	1066
CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG	1108
TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC	1150
TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA	1192
TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG	1234
ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG	1276
GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC	1318
CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA	1360
ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT	1402
GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT	1444
CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA	1486
GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT	1528
AAC ATG TAG	1537
TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG	1587
AGAGTTCATA GCCTACCAGA ACCAACATGC ATCCATTCTT GGCCTGTTAT	1637
ACATTAGTAG AATGGAGGCT ATTTTGTGTTA CTTTTCAAAT GTTTGTTTAA	1687
CTAAACAGTG CTTTTTGCCA TGCTTCTTGT TAACTGCATA AAGAGGTAAC	1737
TGTCACCTGT CAGATTAGGA CTTGTTTTGT TATTTGCAAC AAACCTGGAAA	1787

ACATTATTTT	GTTTTTACTA	AAACATTGTG	TAACATTGCA	TTGGAGAAGG	1837
GATTGTGATG	GCAATGTGAT	ATCATACAGT	GGTGAAACAA	CAGTGAAGTG	1887
GGAAAGTTTA	TATTGTTAAT	TTTGAAAATT	TTATGAGTGT	GATTGCTGTA	1937
TACTTTTTTC	TTTTTTGTAT	AATGCTAAGT	GAAATAAAGT	TGGATTTGAT	1987
GACTTTACTC	AAATTCAATTA	GAAAGTAAAT	CGTAAAACTC	TATTACTTTA	2037
TTATTTTCTT	CAATTATGAA	TTAAGCATTG	GTTATCTGGA	AGTTTCTCCA	2087
GTAGCACAGG	ATCTAGTATG	AAATGTATCT	AGTATAGGCA	CTGACAGTGA	2137
GTTATCAGAG	TCT				2150

(2) INFORMATION FOR SEQUENCE ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: smage-II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCTTATTGG	GTCTGTCTGC	ATATGCCTCC	ACTTGTGTGT	AGCAGTCTCA	50
AATGGATCTC	TCTCTACAGA	CCTCTGTCTG	TGTCTGGCAC	CCTAAGTGGC	100
TTTGCATGGG	CACAGGTTTC	TGCCCTTGCA	TGGAGCTTAA	ATAGATCTTT	150
CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
TACAGGTCTC	TGCCCTTGTA	TGCAGGCCCTA	AGTTTTTCTG	TCTGCTTAGC	250
CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACTTTTG	GAAGTCTGAA	300
ACTAGACTTT	TATGCAGTGG	CCTAACAAGT	TTTAATTTCT	TCCACAGGGT	350
TTGCAGAAAA	GAGCTTGATC	CACGAGTTCG	GAAGTCCTGG	TATGTTCCCTA	400
GAAAGATGTT	CTCCTGGAAA	GCTTCAAAAAG	CCAGGTCTCC	ATTAAGTCCA	450
AGGTATTCTC	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
TCTTTCCAGA	TTCTGTCTG	CCAGCTCTTT	TACTTCAGCC	CTGAGCACAG	550
TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGCAAAACGA	600
CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCACTG	CAGAGGAAGC	650
AGGGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
CTGCTCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTGAG	CACACACTGA	850
AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
AAGTTTAAGA	TGAAAGAAGC	AGTTACAAGG	AGTGAAATGC	TGGCAGTAGT	950
TAACAAGAAG	TATAAGGAGC	AATTCCCTGA	GATCCTCAGG	AGAACTTCTG	1000
CACGCCTAGA	ATTAGTCTTT	GGTCTTGAGT	TGAAGGAAAT	TGATCCCAGC	1050
ACTCATTCCT	ATTTGCTGGT	AGGCAAACTG	GGTCTTTCCA	CTGAGGGAAG	1100
TTTGAGTAGT	AACTGGGGGT	TGCCTAGGAC	AGGTCTCCTA	ATGTCTGTCC	1150
TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	CCACTGAGCA	AGAGGTCTGG	1200
CAATTTCTGC	ATGGAGTGGG	GGTATATGCT	GGGAAGAAGC	ACTTGATCTT	1250
TGGCGAGCCT	GAGGAGTTTA	TAAGAGATGT	AGTGCGGGAA	AATTACCTGG	1300
AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCTGTGG	1350
GGACCCAGAG	CCCATGCTGA	AACAACCAAG	ATGAAAGTCC	TGGAAGTTTT	1400
AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCAGT	1450
TGGCTCTTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500
AAGGGTGTTT	ATTCCAAGGC	CCCATCCCAA	AAGTCTCTTA	ACATGTAGTT	1550
GAGTCTGTTT	TGTTGTGTTT	GAAAAACAGT	CAGGCTCCTA	ATCAGTAGAG	1600
AGTTCATAGC	CTACCAGAAC	CAACATGCAT	CCATTCTTGG	CCTGTTATAC	1650
ATTAGTAGAA	TGGAGGCTAT	TTTTGTTACT	TTTCAAATGT	TTGTTTAACT	1700
AAACAGTGCT	TTTTGCCATG	CTTCTTGTTA	ACTGCATAAA	GAGGTAAGTG	1750
TCACTTGTC	GATTAGGACT	TGTTTTGTGA	TTTGCAACAA	ACTGGAAAAC	1800

ATTATTTTGT TTTTACTAAA ACATTGTGTA ACATTGCATT GGAGAAGGGA	1850
TTGTCATGGC AATGTGATAT CATAcAGTGG TGAAACAACA GTGAAGTGGG	1900
AAAGTTTATA TTGTTAGTTT TGAAAATTTT ATGAGTGTGA TTGCTGTATA	1950
CTTTTTTCTT TTTTGTATAA TGCTAAGTGA AATAAAGTTG GATTTGATGA	2000
CTTTACTCAA ATTcATTAGA AAGTAAATCA TAAAACTCTA TTACTTTATT	2050
ATTTTCTTCA ATTATTAATT AAGcATTGGT TATCTGGAAG TTTCTCCAG	2099

(2) INFORMATION FOR SEQUENCE ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr
5

(2) INFORMATION FOR SEQUENCE ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ACTCAGCTCC TCCCAGATTT 20

(2) INFORMATION FOR SEQUENCE ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GAAGAGGAGG GGCCAAG 17

(2) INFORMATION FOR SEQUENCE ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TCTTGTATCC TGGAGTCC 18

(2) INFORMATION FOR SEQUENCE ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 nucleotides
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTGCCAAGAT CTCAGGAA

18